#5

rFAA

NH₂ ——— Met–Glu–Lys–Leu–Asn–...His–His ——— COOH

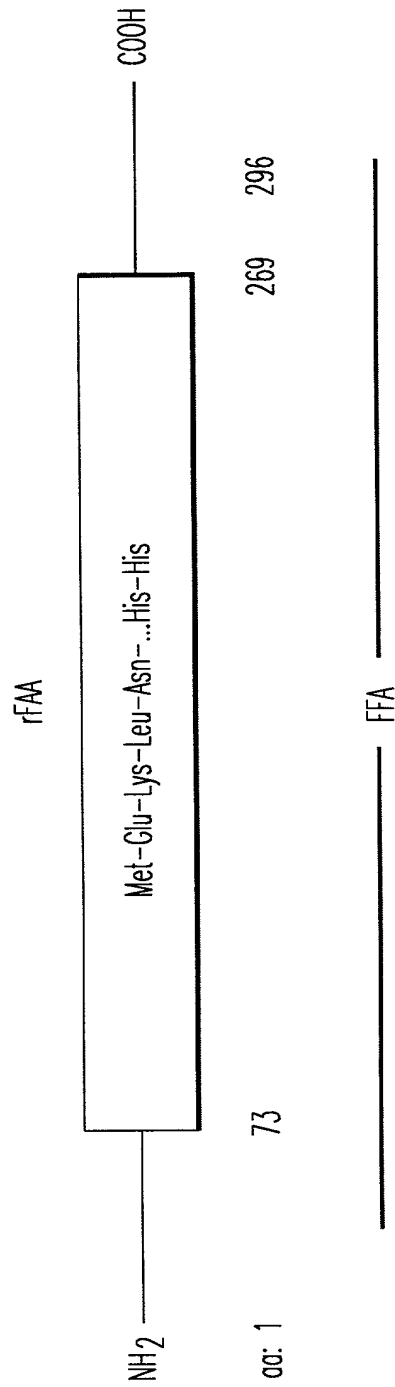aa: 1   73   269   296

FFA

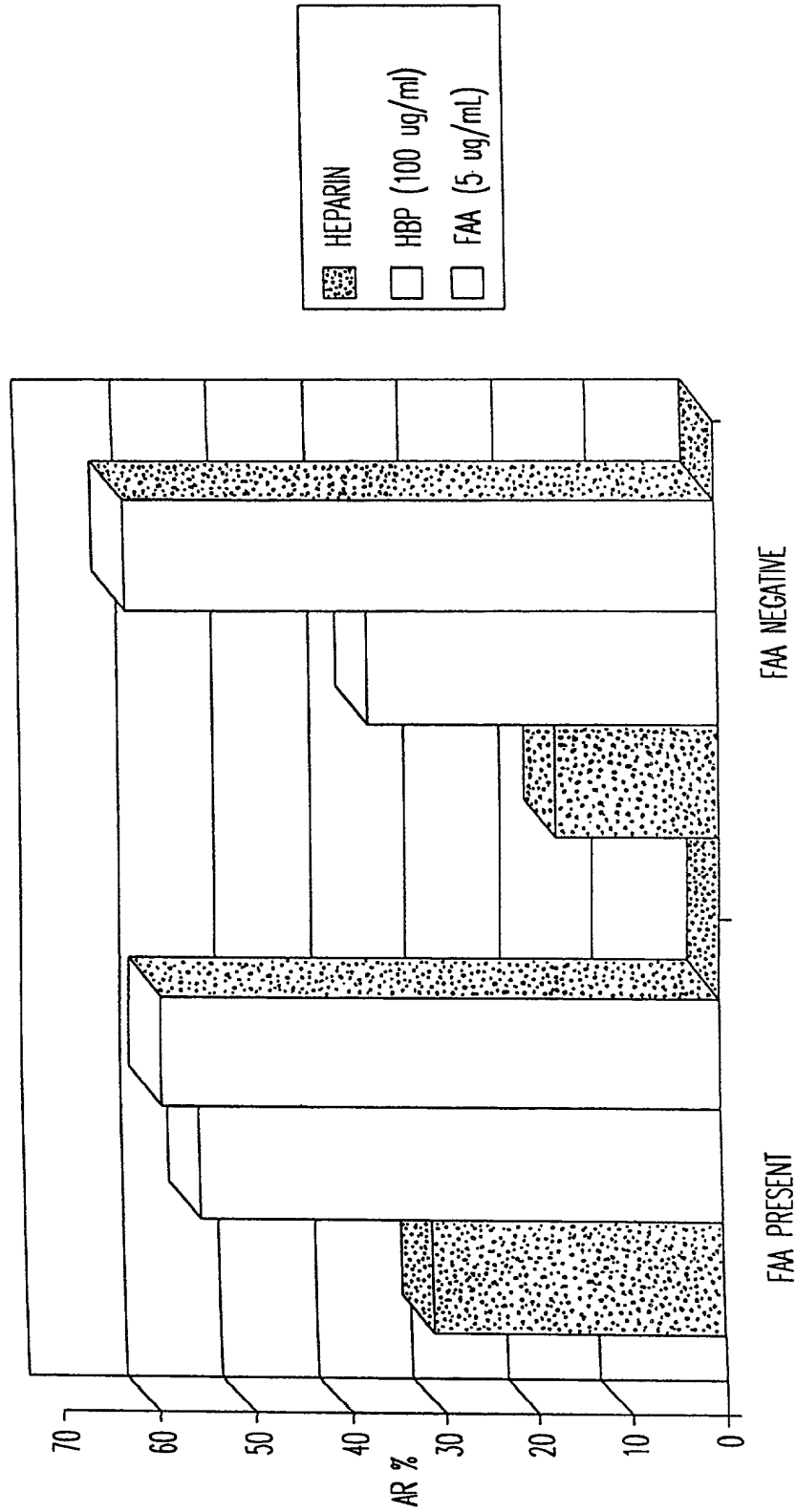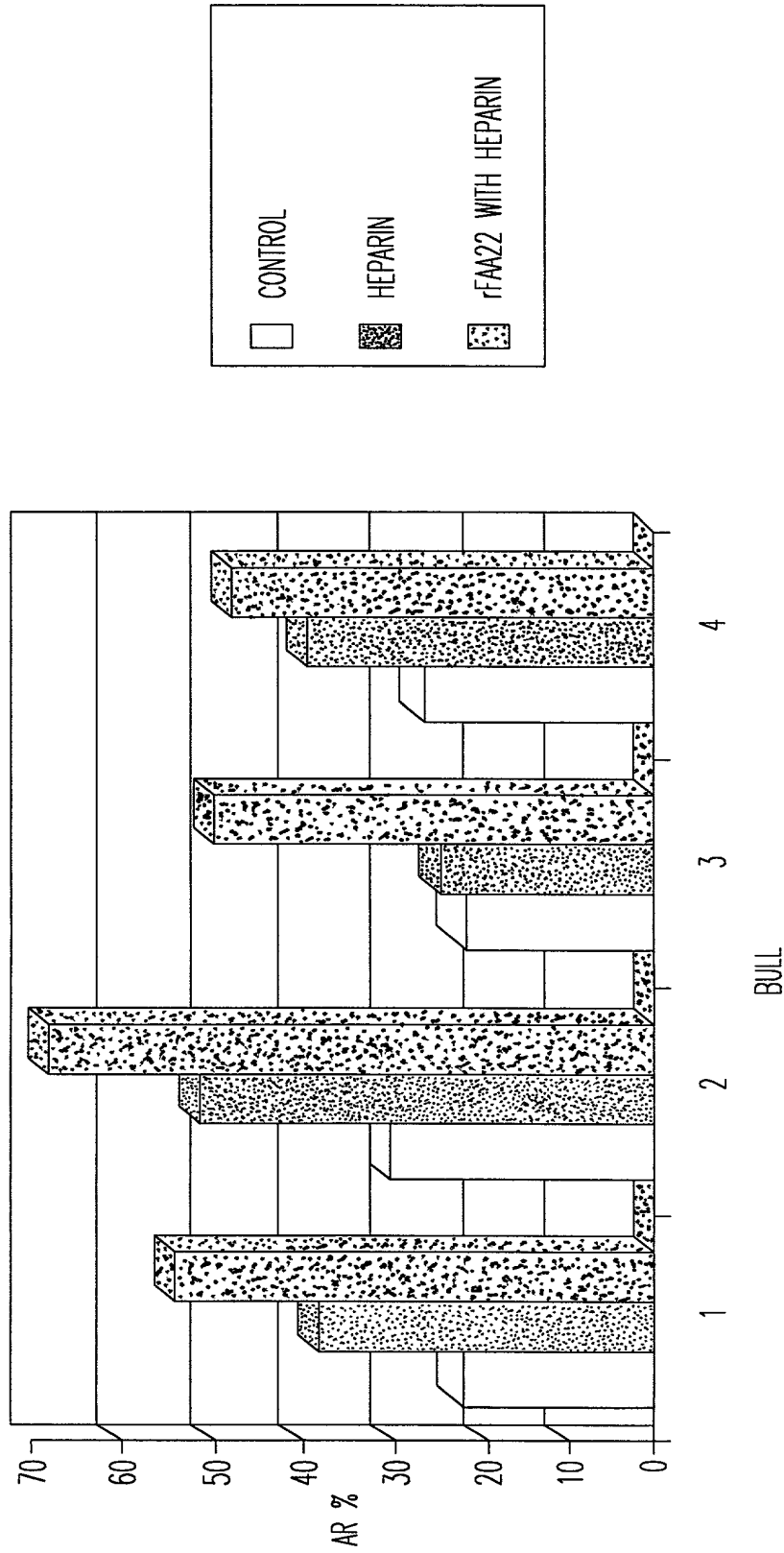*FIG. 1*

FIG.2

FIG. 3

FIG. 4

1 ACAACAGGAT CTGCCCCATA CTGATGGAGA AGCTAAACGG AAATTCAAGA

51 AAAGGCATAA CATACAACTA TGTGATTAGC TCTCGCCTTG GAAGAAACAC

101 ATATAAAGAA CAGTATGCCT TTCTCTATAA AGAAAAGCTA GTGTCTGTAA

151 AACAAAGCTA CCTCTACCAC GACTATCAGG CTGGAGACGC AGATGTGTTT

201 TCCAGGGAAC CCTTTGTGGT CTGGTTCCAG TCACCCTACA CCGCTGTCAA

251 GGACTTCGTG ATTGTCCCCC TGCACACCAC CCCTGAGACA TCCGTTAGAG

301 AGATTGATGA GCTGGCTGAT GTCTACACAG ATGTGAAACG TCGCTGGAAT

351 GCAGAGAATT TCATTTTCAT GGGTGACTTC AATGCTGGCT GCAGCTACGT

401 CCCCAAGAAG GCCTGGAAGG ACATCCGCCT GAGGACGGAC CCCAAGTTCG

451 TTTGGCTGAT CGGGGACCAA GAGGACACCA CGGTCAAGAA GAGCACAAAC

501 TGCGCCTATG ACAGGATCGT GCTTAGAGGA CAAAATATTG TCAACTCTGG

551 TGGTCCTCAA TCAAACCTCG TCTTTGATTT CCAGAAAGCT TACAGGTTGT

601 CTGAATCGAA GGCCCTGGAT GTCAGCGACC ACTTTCCAGT TCATCATCAT

651 CATCATCATG AAGAACCATG A

FIG. 5

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5'    GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC
      1   ---------+---------+---------+---------+---------+---------+    60
a      E  K  L  N  G  N  S  R  K  G  I  T  Y  N  Y  V  I  S  S  R    -


      CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT
      61  ---------+---------+---------+---------+---------+---------+   120
a      L  G  R  N  T  Y  K  E  Q  Y  A  F  L  Y  K  E  K  L  V  S    -


      GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG
      121 ---------+---------+---------+---------+---------+---------+   180
a      V  K  Q  S  Y  L  Y  H  D  Y  Q  A  G  D  A  D  V  F  S  R    -


      GAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACCGCTGTCAAGGACTTCGTGATTGTC
      181 ---------+---------+---------+---------+---------+---------+   240
a      E  P  F  V  V  W  F  Q  S  P  Y  T  A  V  K  D  F  V  I  V    -


      CCCCTGCACACCACCCCTGAGACATCCGTTAGAGAGATTGATGAGCTGGCTGATGTCTAC
      241 ---------+---------+---------+---------+---------+---------+   300
a      P  L  H  T  T  P  E  T  S  V  R  E  I  D  E  L  A  D  V  Y    -


      ACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTTCATGGGTGACTTCAATGCT
      301 ---------+---------+---------+---------+---------+---------+   360
a      T  D  V  K  R  R  W  N  A  E  N  F  I  F  M  G  D  F  N  A    -


      GGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGGACATCCGCCTGAGGACGGACCCCAAG
      361 ---------+---------+---------+---------+---------+---------+   420
a      G  C  S  Y  V  P  K  K  A  W  K  D  I  R  L  R  T  D  P  K    -


      TTCGTTTGGCTGATCGGGGACCAAGAGGACACCACGGTCAAGAAGAGCACAAACTGCGCC
      421 ---------+---------+---------+---------+---------+---------+   480
a      F  V  W  L  I  G  D  Q  E  D  T  T  V  K  K  S  T  N  C  A    -


      TATGACAGGATCGTGCTTAGAGGACAAAATATTGTCAACTCTGGTGGTCCTCAATCAAAC
      481 ---------+---------+---------+---------+---------+---------+   540
a      Y  D  R  I  V  L  R  G  Q  N  I  V  N  S  G  G  P  Q  S  N    -


      CTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG         3'
      541 ---------+---------+---------+---------+-------+--     592
a      L  V  F  D  F  Q  K  A  Y  R  L  S  E  S  K  A  L      -
```
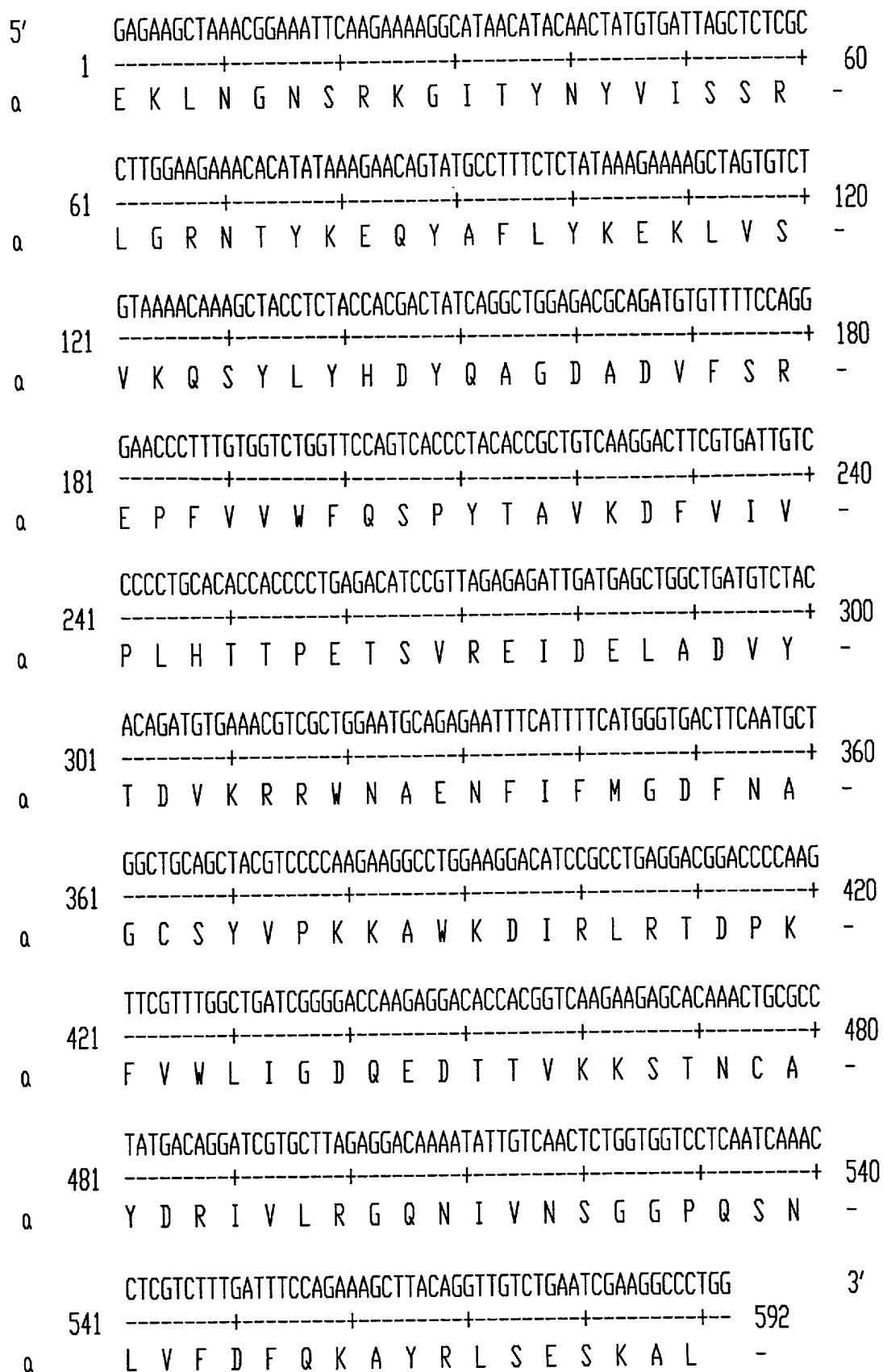
FIG. 6